

51791AUSD1.ST25
SEQUENCE LISTING

<110> Harkins, Richard
Parkes, Deborah
Parry, Gordon
Schneider, Douglas
Steinbrecher, Renate

<120> DNA Encoding a Novel RG-1 Polypeptide

<130> 51791AUSD1

<150> US 60/172,370

<151> 1999-12-16

<150> US 09/732,357

<151> 2000-12-07

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<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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tctccacgt cctatctgcc tctcgctgga ggccaggccg tgcagcatcg aagacaggag      180
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Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala Leu
      5              10              15
ctc ctg gcc act ctc ggc gcc gcc ggc cag cct ctt ggg gga gag tcc      394
Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu Ser
      20              25              30
atc tgt tcc gcc gga gcc ccg gcc aaa tac agc atc acc ttc acg ggc      442
Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr Gly
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aag tgg agc cag acg gcc ttc ccc aag cag tac ccc ctg ttc cgc ccc      490

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Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg Pro	
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Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp Tyr	
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agc atg tgg agg aag aac cag tac gtc agt aac ggg ctg cgc gac ttt	586
Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp Phe	
85 90 95	
gcg gag cgc ggc gag gcc tgg gcg ctg atg aag gag atc gag gcg gcg	634
Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala	
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ggg gag gcg ctg cag agc gtg cac gcg gtg ttt tcg gcg ccc gcc gtc	682
Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val	
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ccc agc ggc acc ggg cag acg tcg gcg gag ctg gag gtg cag cgc agg	730
Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg Arg	
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His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp	
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Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg	
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gaa cag gcg gcg ctg gac ctg tac ccc tac gac gcc ggg acg gac agc	874
Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser	
180 185 190	
ggc ttc acc ttc tcc tcc ccc aac ttc gcc acc atc ccg cag gac acg	922
Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr	
195 200 205	
gtg acc gag ata acg tcc tcc tct ccc agc cac ccg gcc aac tcc ttc	970
Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	
210 215 220 225	
tac tac cca cgg ctg aag gcc ctg cct ccc atc gcc agg gtg aca ctg	1018
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr Leu	
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gtg cgg ctg cga cag agc ccc agg gcc ttc atc cct ccc gcc cca gtc	1066
Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro Val	
245 250 255	
ctg ccc agc agg gac aat gag att gta gac agc gcc tca gtt cca gaa	1114
Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro Glu	
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acg ccg ctg gac tgc gag gtc tcc ctg tgg tcg tcc tgg gga ctg tgc	1162
Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys	
275 280 285	

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 Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr Val
 290 295 300 305

cgg gtc cag ccc gcc aac aac ggg agc ccc tgc ccc gag ctc gaa gaa 1258
 Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu Glu
 310 315 320

gag gct gag tgc gtc cct gat aac tgc gtc taa gaccagagcc ccgcagccccc 1311
 Glu Ala Glu Cys Val Pro Asp Asn Cys Val
 325 330

tggggccccc cggagccatg ggggtgtcggg gggtcctgtg caggctcatg ctgcaggcgg 1371

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Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg
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Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp
 65 70 75 80

Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp
 85 90 95

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Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala
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Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala
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Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg
 130 135 140

Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp
 145 150 155 160

Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp
 165 170 175

Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp
 180 185 190

Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp
 195 200 205

Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser
 210 215 220

Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
 225 230 235 240

Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro
 245 250 255

Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro
 260 265 270

Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu
 275 280 285

Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr
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Leu Phe Arg

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 20 25 30

Val Cys Thr Ala Arg Pro Leu Ala Arg Tyr Ser Ile Thr Phe Thr Gly
 35 40 45

Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg Pro
 50 55 60

Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp Tyr
 65 70 75 80

Ser Met Trp Arg Lys Asn Glu Tyr Val Ser Asn Gly Leu Arg Asp Phe
 85 90 95

Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala
 100 105 110

Gly Glu Lys Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val
 115 120 125

Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val His Pro Arg
 130 135 140

His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp
 145 150 155 160

Phe Val Gly Ile Asp Ser Leu Asp Leu Cys Glu Gly Gly Arg Trp Lys

165

170

175

Glu Gln Val Val Leu Asp Leu Tyr Pro His Asp Ala Gly Thr Asp Ser
 180 185 190

Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr
 195 200 205

Val Thr Glu Ile Thr Ala Ser Ser Pro Ser His Pro Ala Asn Ser Phe
 210 215 220

Tyr Tyr Pro Arg Leu Lys Ser Leu Pro Pro Ile Ala Lys Val Thr Phe
 225 230 235 240

Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ala Pro Pro Ser Leu Asp
 245 250 255

Leu Ala Ser Arg Gly Asn Glu Ile Val Asp Ser Leu Ser Val Pro Glu
 260 265 270

Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys
 275 280 285

Gly Gly Pro Cys Gly Lys Leu Gly Ala Lys Ser Arg Thr Arg Tyr Val
 290 295 300

Arg Val Gln Pro Ala Asn Asn Gly Thr Pro Cys Pro Glu Leu Glu Glu
 305 310 315 320

Glu Ala Glu Cys Ala Pro Asp Asn Cys Val
 325 330